

FIG. 1B

1	GTTTTCAAAA	TCGGTGGAGG	TGCATGAAAA	AGTTATTGGG
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- 41 CATTTTTGA AAATAAAAA ATATCAATAA GTTGGAGTCA ↓START
- 81 TTACCGAATT TTTATACTTA TTTGTTTAGA ATGAACTTTA
 -35
 -10
- 121 TAACATAGTT GGATAGAGTT TTCGATTTAA TACATTAAAT
- 161 GTGAACCTTG CTACAACAAG ATGTGCATCA GA<u>AGGAGTGG</u>
 RIBOSOME BINDING SITE
- 201 TTTAATAATG --sarR--TAA (SEQ ID NO:19)

FIG. 1C

90 100 110
SarR QKRILQDERTVIVYVT-----DTLKANIHKLISELEEY
.:: .::::: SarA KKRNEHDERTVLILVNAQQRKKIESLLSRVNKRITEANNE

SarR IKN (SEQ ID NO:2)

SarA IEL (SEQ ID NO:3)

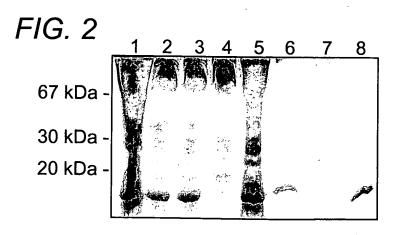


FIG. 3A

FIG. 3B

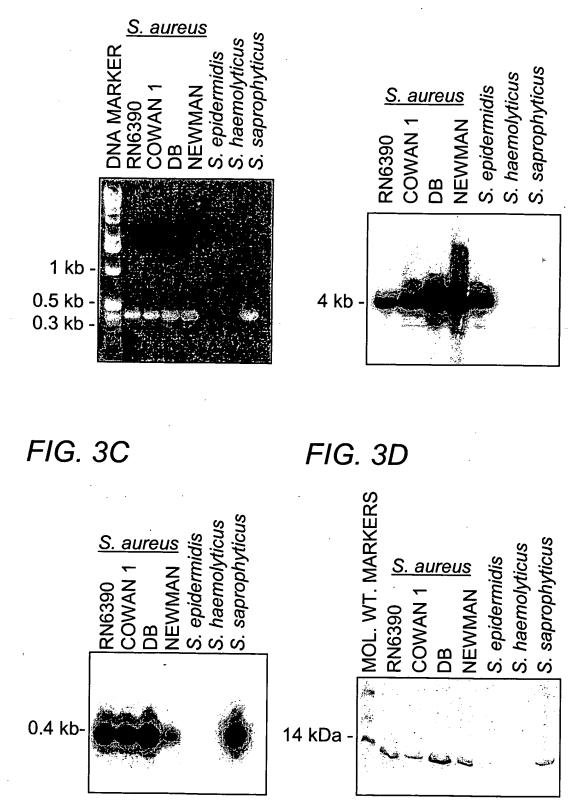


FIG. 4A

FIG. 4B

Sar P1

+

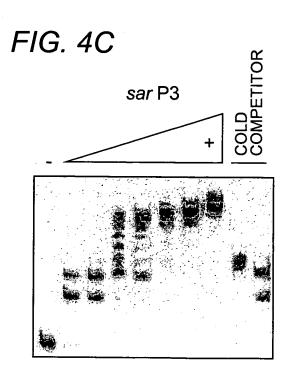
COTO

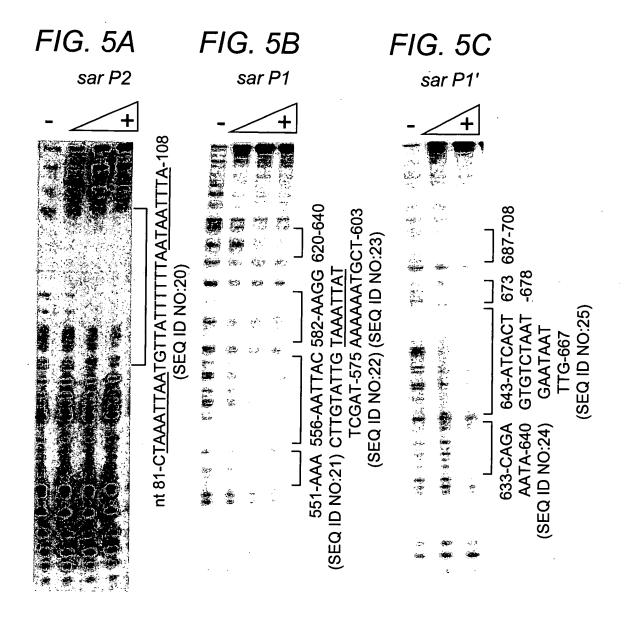
COTO

COTO

COTO

A COTO





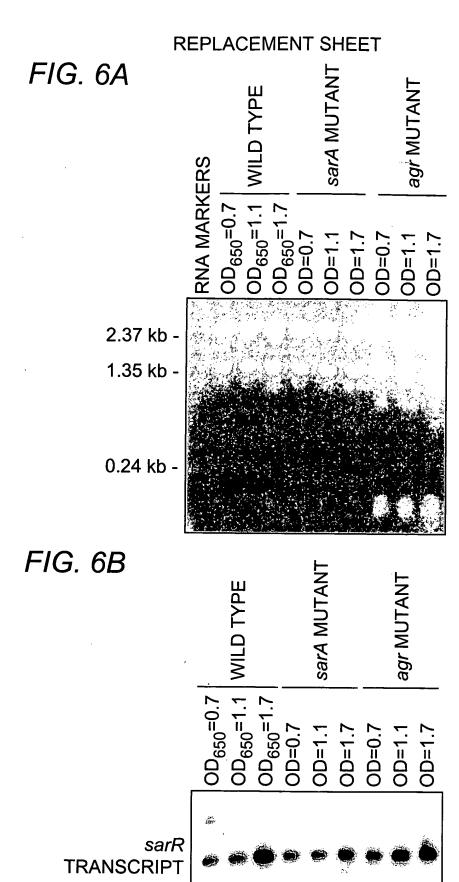


FIG. 6C

OD650nm=1.1 SarK WING OD650nm=1.7 OD650nm=1.7 OD650nm=1.7 CONTROL

FIG. 7A

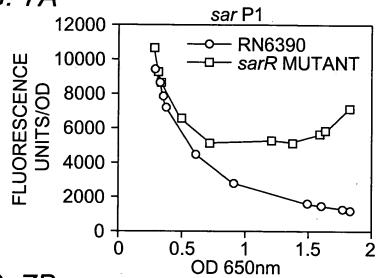


FIG. 7B

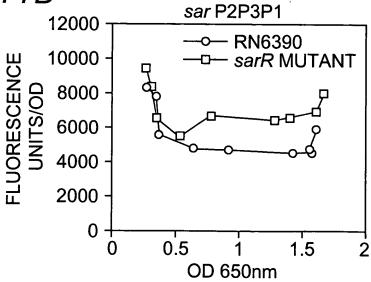


FIG. 8A

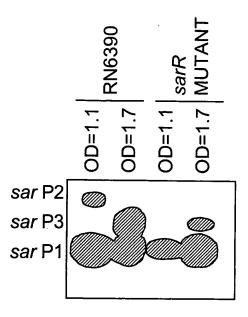


FIG. 8B

	RN6390			sarR MUTANT		, col
OD=0.7	OD=1.1	OD=1.7	OD=0.7	OD=1.1	OD=1.7	+ CONTRO

FIG. 8C

_	OD=1.1	OD=1.7		
	RN6390 sarR MUTANT	RN6390 sarR MUTANT		
RNAII				

FIG. 9A

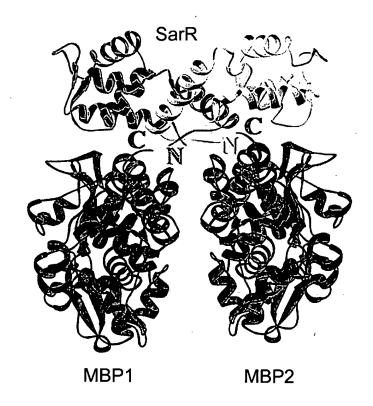
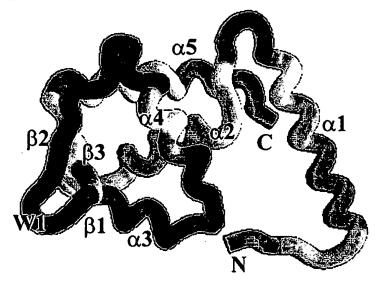
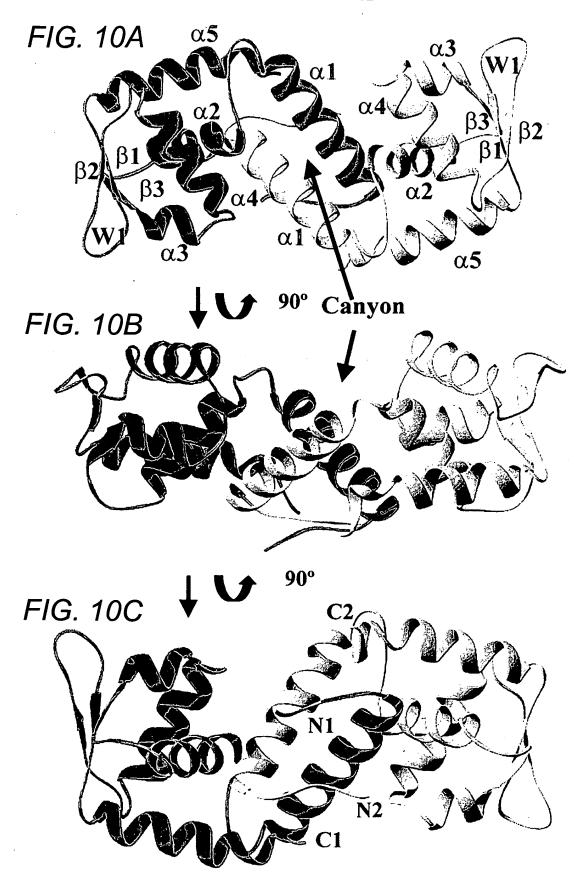
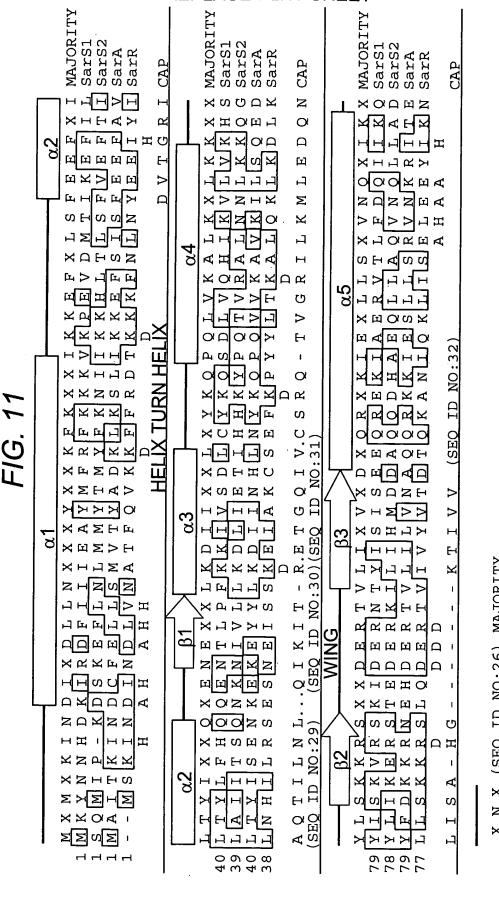


FIG. 9B







X N X (SEQ ID NO:26) MAJORITY 119 F N - (SEQ ID NO:27) SarS1 118 - K D (SEQ ID NO:28) SarS2 119 A N N (SEQ ID NO:35) SarA 117 - - - (SEQ ID NO:2) SarR

FIG. 12A

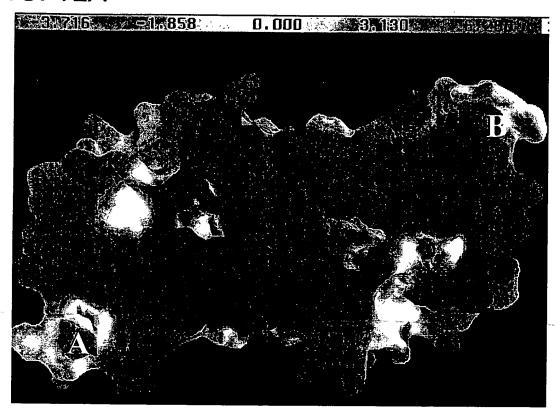


FIG. 12B

